This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images, please do not report the images to the Image Problem Mailbox.

FIGURE 1

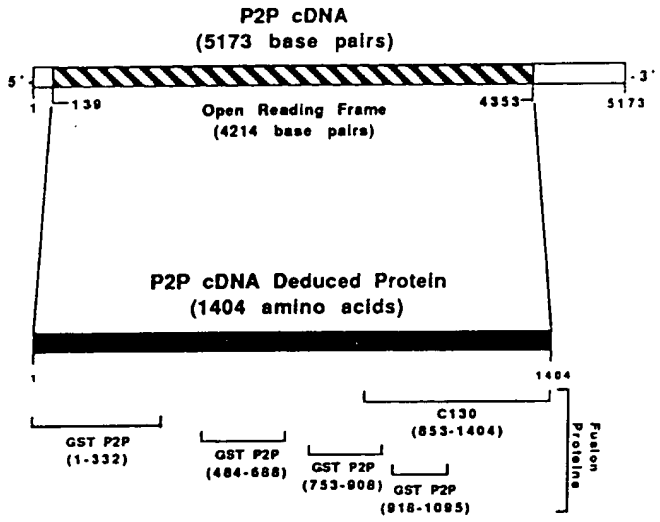

P2P cDNA
(5173 base pairs)
5'
3'
1
139
Open Reading Frame
(4214 base pairs)
4353
5173
P2P cDNA Deduced Protein
(1404 amino acids)
1
1404
C130
(853-1404)
Fusion Proteins
GST P2P
(1-332)
GST P2P
(484-688)
GST P2P
(753-908)
GST P2P
(918-1085)

FIGURE 2

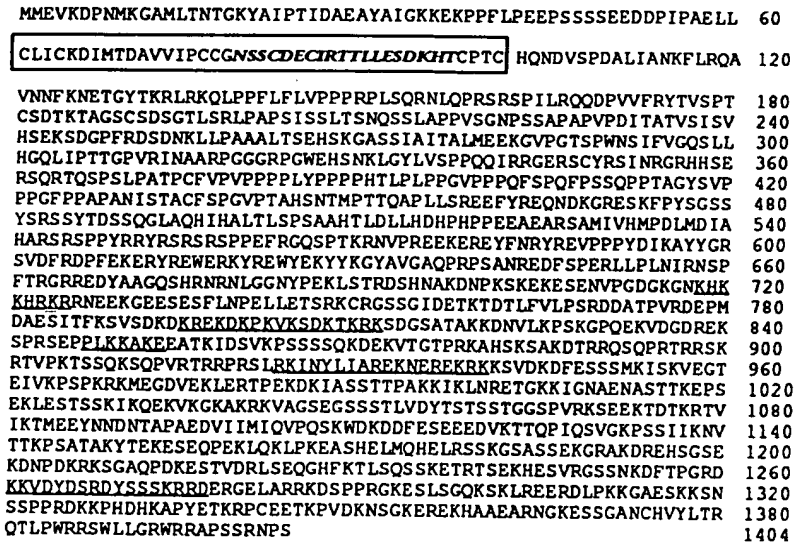

MMEVKDPNMKGAMLTNTGKYAIPTIDAEAYAIGKKEKPPFLPEEPSSSSEEDDPIPAELL 60
CLICKDIMTDAVVIPCCGNSSCDECIRTTLLESDKHTCPTC HQNDVSPDALIANKFLRQA 120
VNNFKNETGYTKRLRKQLPPFLFLVPPPRPLSQRNLQPRSRSPILRQQDPVVFRYTVSPT 180
CSDTKTAGSCSDSGTLSRLPAPSISSLTSNQSSLAPPVSGNPSSAPAPVPDITATVSISV 240
HSEKSDGPFRDSDNKLLPAAALTSEHSKGASSIAITALMEEKGVPGTSPWNSIFVGQSLL 300
HGQLIPTTGPVRINAARPGGGRPGWEHSNKLGYLVSPPQQIRRGERSCYRSINRGRHHSE 360
RSQRTQSPSLPATPCFVPVPPPPLYPPPPHTLPLPPGVPPPQFSPQFPSSQPPTAGYSVP 420
PPGFPPAPANISTACFSPGVPTAHSNTMPTTQAPLLSREEFYREQNDKGRESKFPYSGSS 480
YSRSSYTDSSQGLAQHIHALTLSPSAAHTLDLLHDHPHPPEEAEARSAMIVHMPDLMDIA 540
HARSRSPPYRRYRSRSRSPPEFRGQSPTKRNVPREEKEREYFNRYREVPPPYDIKAYYGR 600
SVDFRDPFEKERYREWERKYREWYEKYYKGYAVGAQPRPSANREDFSPERLLPLNIRNSP 660
FTRGRREDYAAGQSHRNRNLGGNYPEKLSTRDSHNAKDNPKSKEKESENVPGDGKGNKHK 720
KHRKRRNEEKGEESESFLNPELLETSRKCRGSSGIDETKTDTLFVLPSRDDATPVRDEPM 780
DAESITFKSVSDKDKREKDKPKVKSDKTKRKSDGSATAKKDNVLKPSKGPQEKVDGDREK 840
SPRSEPPLKKAKEEATKIDSVKPSSSSQKDEKVTGTPRKAHSKSAKDTRRQSQPRTRRSK 900
RTVPKTSSQKSQPVRTRRPRSLRKINYLIAREKNEREKRKKSVDKDFESSSMKISKVEGT 960
EIVKPSPKRKMEGDVEKLERTPEKDKIASSTTPAKKIKLNRETGKKIGNAENASTTKEPS 1020
EKLESTSSKIKQEKVKGKAKRKVAGSEGSSSTLVDYTSTSSTGGSPVRKSEEKTDTKRTV 1080
IKTMEEYNNDNTAPAEDVIIMIQVPQSKWDKDDFESEEEDVKTTQPIQSVGKPSSIIKNV 1140
TTKPSATAKYTEKESEQPEKLQKLPKEASHELMQHELRSSKGSASSEKGRAKDREHSGSE 1200
KDNPDKRKSGAQPDKESTVDRLSEQGHFKTLSQSSKETRTSEKHESVRGSSNKDFTPGRD 1260
KKVDYDSRDYSSSKRRDERGELARRKDSPPRGKESLSGQKSKLREERDLPKKGAESKKSN 1320
SSPPRDKKPHDHKAPYETKRPCEETKPVDKNSGKEREKHAAEARNGKESSGANCHVYLTR 1380
QTLPWRRSWLLGRWRRAPSSRNPS 1404

FIGURE 3

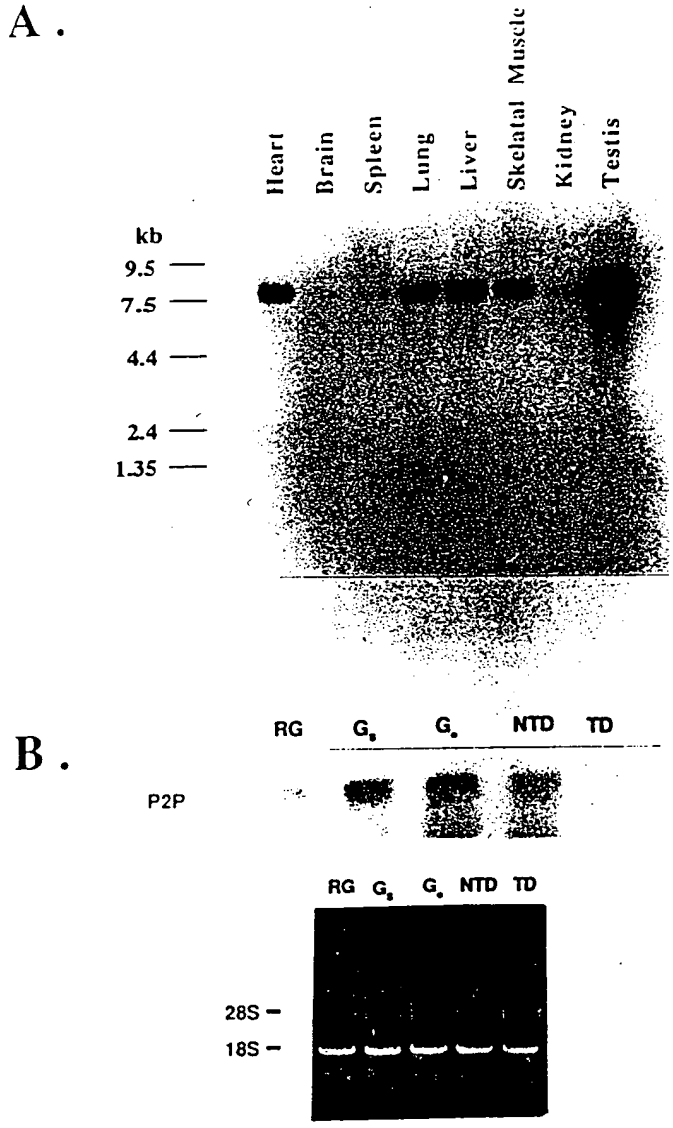
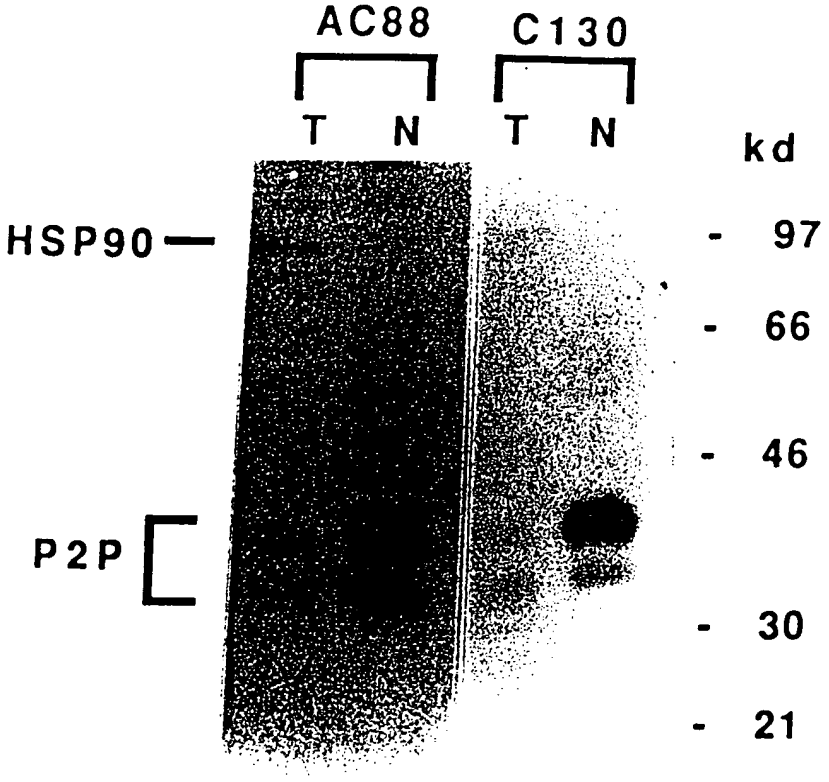
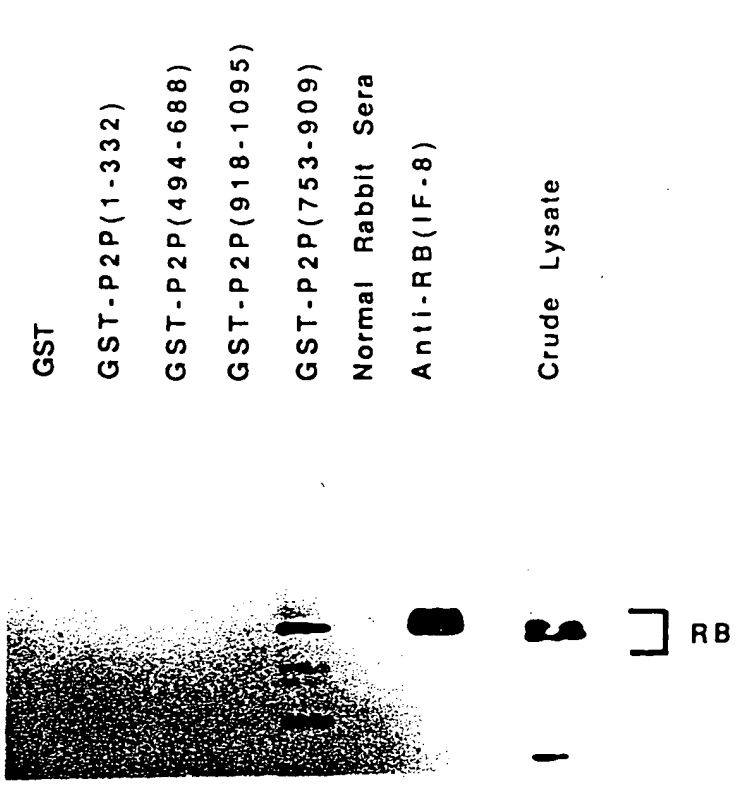

A.
Heart
Brain
Spleen
Lung
Liver
Skelatal Muscle
Kidney
Testis
kb
9.5
7.5
4.4
2.4
1.35
B.
RG
G0
G1
NTD
TD
P2P
RG G0 G1 NTD TD
28S
18S

FIGURE 4





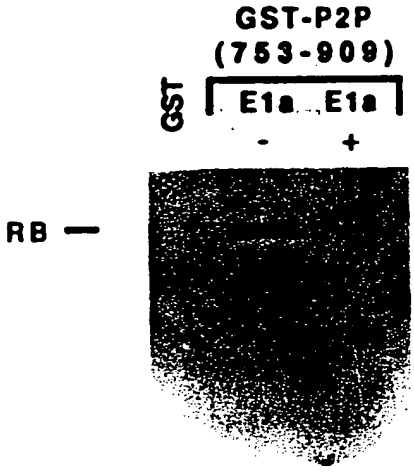


Fig. 5

0694570 .0694401

0041045.0641401

```
                                                                  60
                                                                   *
AGGTCCACCACCTCCATCTTACACCTGCTTTCGTTGTGGTAAACCTGGTCATTATATTAAGAAT
                                                                 120
                                                                  *
TGCCAACAAATGGGGATAAGAACTTTGAATCTGGTCCTAGGATCAAAAAGAGCACTGGAATTCC
                                                        180
                                                         *
TAGAAGTTTTATGATGGAAGTGAAAGATCCTAACATGAAAGGTGCAATGCTTACCAACACTGGA
                                                    240
                                                     *
AAATATGCAATACCAACTATAGATGCAGAGGCCTATGCAATCGGGAAGAAAGAGAAACCACCCT
                                                300
                                                 *
TCTTACCAGAGGAGCCATCATCATCTTCAGAAGAAGATGATCCTATCCCAGCAGAGCTCTTGTG
                                            360
                                             *
CCTCATCTGCAAAGACATCATGACTGATGCTGTGGTCATTCCCTGCTGTGGAAACAGTTCATGT
                                        420
                                         *
GATGAATGTATAAGAACGACACTCTTGGAGTCAGATAAACATACATGTCCAACATGTCACCAAA
                                    480
                                     *
ATGATGTTTCTCCTGATGCTTTAATTGCCAACAAGTTTTTACGACAGGCTGTTAATAACTTTAA
                                540
                                 *
AAATGAAACTGGCTATACAAAACGACTACGAAAACAGTTACCTCCATTTTTATTTTTAGTACCA
                            600
                             *
CCACCAAGACCACTCAGTCAGCGGAACCTACAGCCTCGTAGTAGATCTCCAATACTAAGACAGC
                        660
                         *
AGGATCCTGTAGTATTCAGGTACACTGTCTCGCCTACCTGCTCCGATACTAAGACAGCAGGATC
                    720
                     *
CTGTAGTGATTCAGGTACACTGTCTCGCCTACCTGCTCCGTCTATATCTTCATTAACTTCTAAT
                780
                 *
CAGTCTTCCTTGGCCCCTCCTGTGTCTGGAAATCCGTCTTCTGCTCCAGCTCCAGTACCTGATA
            840
             *
TAACTGCAACCGTGTCTATATCAGTCCACTCAGAAAAATCGGATGGACCTTTTCGGGATTCTGA
900                                                             960
 *                                                               *
TAATAAATTATTGCCAGCTGCCGCCCTTACATCAGAACATTCAAAGGGAGCCTCTTCAATTGCT
                                                            1020
                                                             *
ATTACTGCTCTTATGGAAGAAAAAGGGGTACCAGGTACCAGTCCTTGGAACTCCATCTTTGTTG
```

Fig. 6A

0621104545 - 062104

```
                                                                1080
                                                                 *
GACAGTCATTATTACATGGACAGTTGATTCCCACAACTGGCCCAGTAAGAATCAATGCTGCTCG
                                                          1140
                                                           *
TCCAGGTGGTGGCCGGCCAGGCTGGGAGCATTCCAACAAGCTTGGGTACCTAGTTTCTCCACCA
                                                    1200
                                                     *
CAGCAAATTAGAAGAGGAGAAAGAAGCTGTTACAGAAGTATAAACCGCGGGCGACACCACAGCG
                                                1260
                                                 *
AACGATCACAGAGGACTCAAAGCCCATCACTTCCAGCAACTCCATGCTTTGTGCCCGTTCCACC
                                            1320
                                             *
ACCTCCTTTGTATCCGCCTCCTCCCCATACACTTCCTCTTCCTCCAGGTGTACCTCCTCCACAG
                                        1380
                                         *
TTTTCTCCTCAGTTTCCCTCCTCCCAGCCTCCAACAGCAGGATATAGTGTCCCTCCTCCAGGAT
                                    1440
                                     *
TTCCACCAGCTCCTGCCAATATATCAACAGCTTGCTTTTCACCAGGTGTTCCCACTGCCCATTC
                                1500
                                 *
AAATACCATGCCCACAACACAAGCACCTCTTTTGTCCAGGGAAGAATTCTATAGAGAGCAAAAC
                            1560
                             *
GACAAAGGAAGAGAGTCTAAATTTCCCTATAGTGGGTCATCGTATTCAAGAAGTTCATACACTG
                        1620
                         *
ACTCAAGTCAAGGTCTGGCTCAACACATTCACGCTCTTACTCTCAGTCCTTCAGCTGCTCACAC
                    1680
                     *
TCTCGATCTTCTTCACGATCATCCCCATCCTCCAGAAGAGGCAGAGGCAAGATCTGCAATGATT
                1740
                 *
GTTCACATGCCAGATCTCATGGATATCGCCCATGCTAGGTCAAGGTCACCTCCCTATAGACGAT
            1800
             *
ATCGCTCACGGTCCAGATCTCCTCCAGAATTTAGGGGACAGTCTCCCACTAAACGTAATGTACC
1860                                                                1920
 *                                                                   *
TCGAGAAGAGAAAGAACGTGAGTATTTTAATAGATACAGAGAAGTTCCACCCCCTTATGACATC
                                                                1980
                                                                 *
AAAGCCTATTATGGGCGGAGTGTCGACTTTAGAGACCCATTTGAGAAAGAACGCTACCGGGAAT
                                                            2040
                                                             *
GGGAAAGGAAATACCGAGAGTGGTATGAGAAGTACTACAAAGGGTACGCGGTGGGAGCTCAACC
```

Fig. 6B

0961150 - 0961404

```
                                                                2100
                                                                 *
TAGACCCTCAGCCAATAGAGAGGACTTTTCTCCAGAGAGACTCTTACCTCTTAATATCAGAAAT
                                                          2160
                                                           *
TCACCCTTCACAAGAGGCCGCAGAGAAGACTATGCTGCTGGACAAAGTCATAGAAATAGAAATC
                                                     2220
                                                      *
TAGGTGGCAACTATCCAGAAAAGCTTTCAACAAGGGACAGTCACAATGCAAAAGATAATCCAAA
                                               2280
                                                *
ATCGAAGGAGAAGGAGAGTGAGAATGTTCCAGGAGACGGCAAAGGGAACAAGCATAAGAAACAC
                                          2340
                                           *
AGGAAACGAAGAAACGAAGAAAAGGGGGAAGAGAGTGAGAGCTTCCTGAACCCAGAGCTACTGG
                                     2400
                                      *
AGACGTCTAGGAAATGCAGGGGATCGTCAGGGATTGATGAAACGAAGACAGATACACTGTTTGT
                                2460
                                 *
TCTCCCAAGCAGAGACGATGCTACACCTGTTAGGGATGAGCCAATGGACGCAGAATCGATCACT
                           2520
                            *
TTCAAGTCAGTATCTGACAAAGACAAGAGGGAAAAGGATAAGCCAAAAGTAAAAAGTGACAAGA
                       2580
                        *
CCAAACGGAAAAGTGACGGGTCTGCTACAGCCAAGAAAGACAATGTTTTAAAACCTTCTAAAGG
                  2640
                   *
ACCTCAAGAAAAGGTAGATGGAGACCGTGAAAAGTCTCCTCGGTCTGAGCCGCCACTCAAAAAA
             2700
              *
GCCAAAGAGGAGGCTACAAAGATTGACTCTGTAAAACCTTCCTCGTCTTCTCAGAAGGATGAGA
        2760
         *
AGGTCACTGGAACCCCTAGAAAAGCCCATTCTAAATCTGCAAAAGACACCAGGAGGCAAAGCCA
2820                                                          2880
 *                                                             *
GCCAAGGACGAGAAGGTCAAAAAGGACTGTTCCAAAGACATCAAGTCAGAAAAGCCAGCCAGTA
                                                         2940
                                                          *
AGGACGAGAAGGCCAAGAAGCCTGAGAAAAATAAACTACTTGATAGCAAGGGAGAAAAACGAAA
                                                    3000
                                                     *
GAGAAAAACGGAAGAAGAGTGTAGATAAAGATTTTGAGTCGTCTTCAATGAAAATCTCTAAAGT
```

Fig. 6C

0960745 0960745

```
                                                          3060
                                                            *
AGAAGGAACAGAAATAGTGAAACCATCACCAAAACGGAAAATGGAAGGTGATGTTGAAAAGCTG
                                                    3120
                                                      *
GAAAGGACCCCAGAAAAGGACAAGATTGCATCATCAACTACTCCAGCCAAAAAAATCAAACTCA
                                                3180
                                                  *
ACAGAGAAACTGGAAAAAAAATTGGAAATGCAGAAAATGCATCTACTACAAAAGAACCCTCTGA
                                            3240
                                              *
AAAATTGGAGTCAACATCTAGCAAAATCAAACAGGAAAAAGTCAAGGGAAAGGCCAAACGGAAA
                                        3300
                                          *
GTAGCTGGGTCGGAAGGCTCCAGCTCCACGCTTGTGGATTACACCAGTACAAGTTCAACTGGAG
                                    3360
                                      *
GCAGTCCTGTGAGGAAATCTGAAGAAAAGACAGATACAAAGCGAACAGTCATTAAAACTATGGA
                               3420
                                 *
GGAATATAATAATGATAACACAGCTCCTGCTGAAGATGTTATAATTATGATCCAGGTTCCTCAG
                           3480
                             *
TCCAAATGGGATAAAGATGACTTTGAGTCTGAAGAAGAAGATGTTAAAACCACACAACCTATAC
                       3540
                         *
AGAGTGTAGGGAAACCATCGAGTATTATAAAAAATGTCACTACTAAGCCATCGGCTACGGCTAA
                   3600
                     *
GTACACCGAGAAGGAAAGCGAGCAGCCCGAGAAACTGCAGAAGCTTCCCAAGGAGGCGAGCCAC
              3660
                *
GAGCTGATGCAGCACGAGCTCAGGAGCTCAAAGGGCAGTGCGTCCAGTGAGAAGGGCAGAGCCA
         3720
           *
AGGACCGGGAGCACTCAGGGTCGGAGAAGGACAACCCTGACAAGAGGAAGAGCGGTGCCCAGCC
3780                                                              3840
  *                                                                 *
AGACAAGGAGAGCACTGTGGACCGCCTGAGTGAGCAGGGACATTTTAAGACTCTCTCTCAGTCT
                                                                3900
                                                                  *
TCCAAAGAGACCAGGACTTCAGAGAAGCACGAGTCTGTTCGTGGTTCCTCAAATAAAGACTTCA
                                                          3960
                                                            *
CTCCTGGTAGAGACAAGAAAGTGGACTACGACAGCAGGGATTATTCCAGTTCCAAGCGAAGAGA
                                                      4020
                                                        *
CGAGAGAGGTGAATTAGCAAGGAGAAAAGACTCTCCTCCCCGGGGCAAAGAGTCTCTGTCTGGG
```

Fig. 6D

```
                                                        4080
                                                         *
CAGAAAAGCAAGCTGAGGGAGGAGAGAGATTTACCTAAAAAGGGGGCCGAGTCAAAAAAAAGTA
                                                   4140
                                                    *
ATTCTAGCCCCCCAAGAGACAAAAAGCCTCATGATCATAAAGCCCCCTACGAAACTAAACGCCC
                                              4200
                                               *
ATGTGAAGAGACAAAGCCTGTAGATAAAAACTCTGGGAAGGAGCGGGAGAAGCATGCTGCTGAA
                                         4260
                                          *
GCTCGCAATGGGAAAGAGTCCAGTGGTGCAAACTGCCATGTATACCTAACCCGCCAGACCCTCC
                                    4320
                                     *
CATGGAGAAGGAGCTGGCTGCTGGGCAGGTGGAGAAGAGCGCCGTCAAGCCGAAACCCCAGCTG
                               4380
                                *
AGCCATTCCTCGAGGCTTTCCTCTGACCTGACCCGGGAGACGAACGAGGCAGCCTTTGAACCAG
                          4440
                           *
ATTATAATGAGAGCGACAGTGAGAGTAATGTGTCTGTGAAGGAAGAAGAAGCTGTTGCCAGTAT
                     4500
                      *
CTCCAAGGACTTGAAAGAGAAAACAACAGAGAAAGCGAAAGAGAGCTTGACTGTAGCAACGGCC
                4560
                 *
AGCCAGCCAGGTGCAGACAGGAGCCAGAGCCAAAGTAGCCCAGTGTTAGTCAGTAGAGTCATAG
           4620
            *
CCTTCGGAGCCAGACCCGAAGCCACAGCAGCAGTGCCAGCTCAGCCGGAAGGCCAGGACAGCAA
      4680
       *
AAAGAAGAAGAAGAAGAAGGAGAAGAAAAACGACAAGAAGCATAAAAAGCACAAGAAGCACAAG
4740                                                              4800
  *                                                                *
AAGCACGCAGGCCGACGGCGACGTGGAGAAGAGCCAGAAACACAAACACAAGAAGAAGAAGGCC
                                                              4860
                                                               *
AAGAAGAACAAAGACAAGGAGAAGGAGAAAGATGACCAAAAAGTGAGATCTGTCACTGTGTGAA
                                                         4920
                                                          *
GGACGGATGTGTTAATTGACTTAATTACTAAGTCATCTGTATTAAATTCTGTTATAATGTAAAG
                                                    4980
                                                     *
AGATTCCAGCCTTGTAAATAATGAATGGAAGACCCTGTGCTGCACTTAAAAGTATTTGCTGCTT
                                                5040
                                                 *
GATTATTTCATTTTTACATCAGAGCTTTATAACGAACTTTTGTACAGAATTGTGAGTTGTGACC
```

Fig. 6E

0960740.0960450

5100
*
ATGGAACAGTGAGAGGTTTTGCTAGGGCCTATTATTTTTAACCACCATTAATTAGTTGGGGTGG
5160
*
AGTTTACTGTACTGTGAAATTTTCACATTTGAATTTTTTTAATTGCCTGGCAA

09817045-061401

Fig. 6F